

Supplementary Table 2. Significantly enriched pathways detected in pathway enrichment analysis and targets prediction (Diana mirPath v.3 web-based computational tool) of the 66* upregulated miRNAs in metastatic tumors compared to those in normal surrounding liver.

KEGG pathway	p-value
1. Fatty acid biosynthesis (hsa00061)	<1e-325
2. Prion diseases (hsa05020)	<1e-325
3. ECM-receptor interaction (hsa04512)	<1e-325
4. Adherens junction (hsa04520)	1.893252e-11
5. Viral carcinogenesis (hsa05203)	2.014489e-11
6. Proteoglycans in cancer (hsa05205)	2.625722e-11
7. Hippo signaling pathway (hsa04390)	8.28115e-10
8. Cell cycle (hsa04110)	8.251494e-07
9. Lysine degradation (hsa00310)	2.515057e-06
10. Protein processing in endoplasmic reticulum	1.718417e-05
11. Hepatitis B (hsa05161)	3.304304e-05
12. p53 signaling pathway (hsa04115)	6.020478e-05
13. Fatty acid metabolism (hsa01212)	0.0001324588
14. Pathways in cancer (hsa05200)	0.0003046663
15. Chronic myeloid leukemia (hsa05220)	0.001297946
16. TGF-beta signaling pathway (hsa04350)	0.007290645
17. Glioma (hsa05214)	0.008409624
18. Thyroid hormone signaling pathway (hsa04919)	0.02322047

*Of the 73 miRNAs shown in Table 1, four miRNAs (miR-378d, miR-378a-5p, miR-146b-3p and miR-203a) were downregulated in tumors. Out of the rest 69 miRNAs, three miRNAs (miR-127-3p, miR-543 and miR-127-5p) were excluded because they were not recognized by Diana mirPath v.3 web-based computational tool.